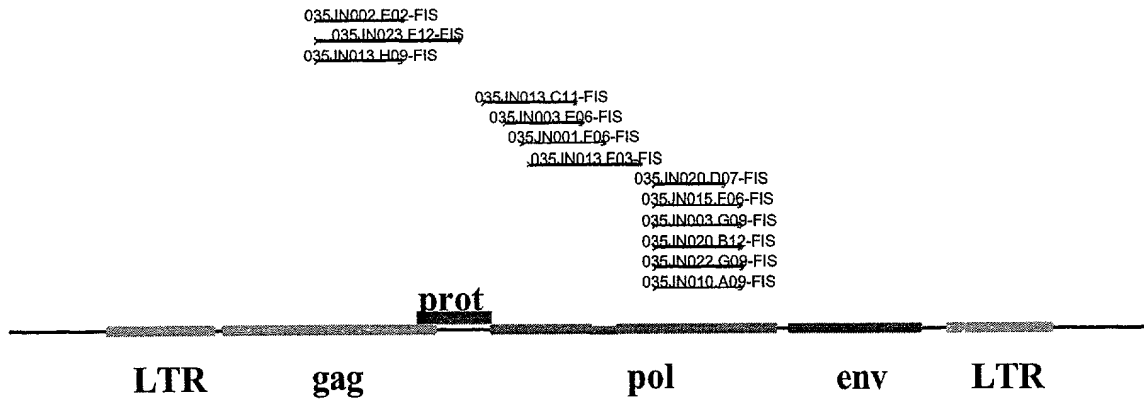
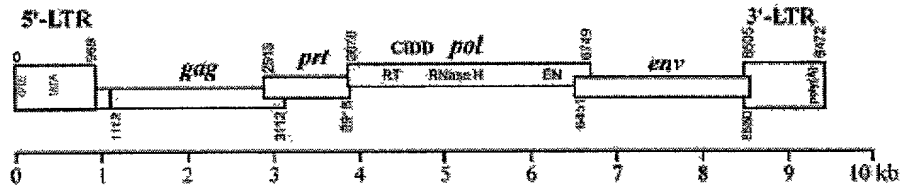
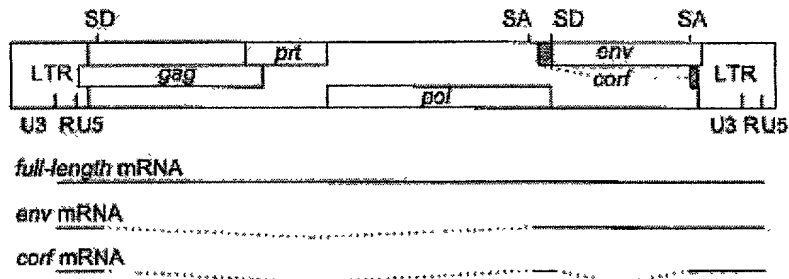


FIGURE 1**FIGURE 2****FIGURE 3**

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FIGURE 4

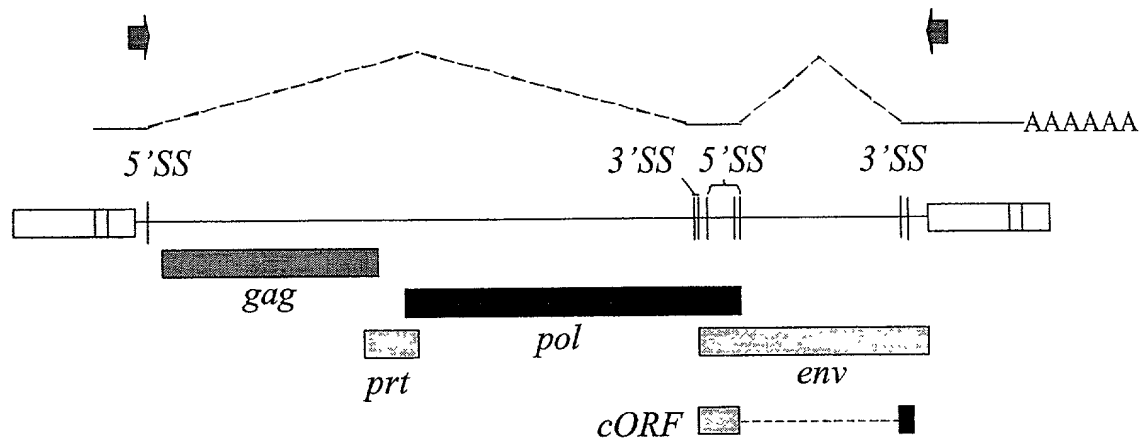


FIGURE 5

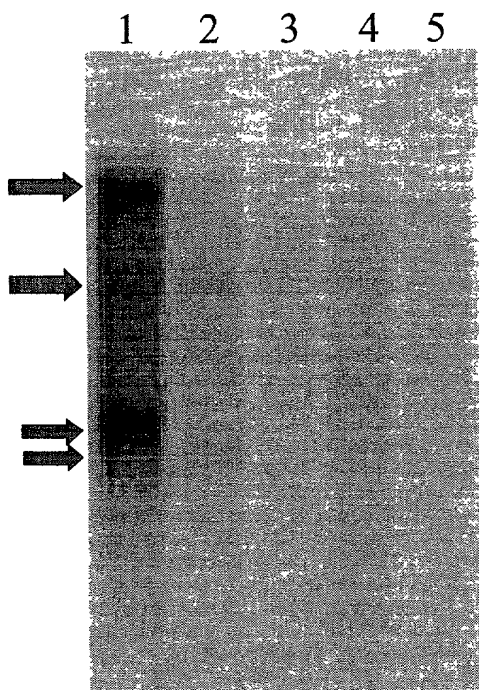


FIGURE 6

ENV GENOMIC HERV MDA	(1)	-----	GAATTTGAAGTTCTTACA	80
ENV GENOMIC HERV-K TAN.	(1)	-----	AGATTGAACTTCTACA	
ENV GENOMIC AC025420	(1)	-----	ACATTGAACTTCTACA	
ENV GENOMIC AF000776	(1)	-----	ACATTGAACTTCTACA	
ENV GENOMIC HERV-K8	(1)	-----	-----	
ENV GENOMIC HERV-KI	(1)	-----	ACATTGAACTTCTACA	
ENV HERV-K AF023261	(1)	GGGGAGAGGTTTGTCTTGTGTTTCCACGAGGAGAAATCAGCTTCCTGTTGGATACCCACTAGCACTTTGAGTTCTACA		
ENV GEN AL035086	(1)	-----	-----	
ENV GENOMIC AL035587	(1)	-----	AAATTGAAGTTCTACA	
ENV GENOMIC AC012068	(1)	-----	-----	
ENV GENOMIC AF277315	(1)	-----	TTTAAAGTTCTACA	
ENV GENOMIC AF027650	(1)	GGGGAGAGGTTTGTCTTGTGTTTCCACGAGGAGAAATCAGCTTCCTGTTGGATACCCACTAGCACTTTGAGTTCTACA		
ENV GENOMIC AC078899	(1)	-----	-----	
ENV GENOMIC HERV-KII	(1)	-----	ACATTGAACTTCTACA	
ENV GENOMIC AC008813	(1)	-----	ATACCCACTAGCACTTAAAGTTCTACA	
ENV GENOMIC AC012309	(1)	-----	TAGCACTTGAAGTTCTACA	
ENV GENOMIC AL121932	(1)	-----	ACATTGAACTTCTACA	
ENV GENOMIC AD000090	(1)	-----	ACATTGAACTTCTACA	
ENV GEN AL160008	(1)	-----	-----	
ENV GENOMIC HB32496	(1)	---GCGTAATCATTGAGGACAAGTCGACGAGAGATCCGAGGACGCTCTACAGTCAGCCTTACGCACTTTGAGTTCTACA		
ENV GENOMIC AC011467	(1)	-----	GGTTTGTGCTTGTGTTTCCACGAGGAGA-AAATCAGCTTCCTGTTGGATGCCCCACTAGCACTTTGAGTTCTACA	
ENV GENOMIC AF235103	(1)	-----	TTTTCTTGTGTTTCCACGAGGAGA-AAATCAGCTTCCTGTTGGATACCCACTAGCACTTTGAGTTCTACA	
ENV GENOMIC AC026786	(1)	-----	TTTTGCTTGTGTTTAAACGAGAAATAAATCAGCTTCCTGTTGGATACCTTACAATT	
ENV GENOMIC AC034203	(1)	-----	-----	
ENV GENOMIC AC018809	(1)	-----	-----	
ENV GENOMIC HERV-KI02 AF164610	(1)	-----	TTGCTTGTGTTTCCACGAGGAGA-AAATCAGCTTCCTGTTGGATACCCACTAGCACTTTGAGTTCTACA	
ENV GENOMIC FRAG. AF260253	(1)	-----	-----	
CONSENSUS	(1)	-----	ACATTGAACTTCTACA	
ENV GENOMIC HERV MDA	(18)	ATGAACCTATCTGAGATGCAAGAA	ATT-----GTGAGATGAGTCAAGCTTATGGA	160
ENV GENOMIC HERV-K TAN.	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC025420	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AF000776	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC HERV-K8	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC HERV-KI	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV HERV-K AF023261	(81)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GEN AL035086	(1)	-----	-----	
ENV GENOMIC AL035587	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC012068	(6)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AF277315	(15)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AF027650	(79)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC078899	(16)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC HERV-KII	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC008813	(29)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC012309	(21)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AL121932	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AD000090	(18)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GEN AL160008	(1)	-----	-----	
ENV GENOMIC HB32496	(78)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC011467	(74)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AF235103	(72)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC026786	(58)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC034203	(58)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC AC018809	(16)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC HERV-KI02 AF164610	(70)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC FRAG. AF260253	(1)	-----	-----	
CONSENSUS	(81)	ATGAACCTATCTGAGATGCAAGAA	ATGAACCTGAGTCAAGCTTATGGA	
ENV GENOMIC HERV MDA	(72)	-----	-----	240
ENV GENOMIC HERV-K TAN.	(83)	-----	-----	
ENV GENOMIC AC025420	(83)	-----	-----	
ENV GENOMIC AF000776	(83)	-----	-----	
ENV GENOMIC HERV-K8	(15)	-----	-----	
ENV GENOMIC HERV-KI	(83)	-----	-----	
ENV HERV-K AF023261	(146)	-----	-----	
ENV GEN AL035086	(1)	-----	-----	
ENV GENOMIC AL035587	(83)	-----	-----	
ENV GENOMIC AC012068	(71)	-----	-----	
ENV GENOMIC AF277315	(80)	-----	-----	
ENV GENOMIC AF027650	(144)	-----	-----	
ENV GENOMIC AC078899	(81)	-----	-----	
ENV GENOMIC HERV-KII	(72)	-----	-----	
ENV GENOMIC AC008813	(104)	-----	-----	
ENV GENOMIC AC012309	(86)	-----	-----	
ENV GENOMIC AL121932	(83)	-----	-----	
ENV GENOMIC AD000090	(88)	CGAGAACCACTGAGTCAAGCTTATGGA	CGAGAACCACTGAGTCAAGCTTATGGA	
ENV GEN AL160008	(1)	-----	-----	
ENV GENOMIC HB32496	(143)	-----	-----	
ENV GENOMIC AC011467	(128)	-----	-----	
ENV GENOMIC AF235103	(142)	-----	-----	
ENV GENOMIC AC026786	(58)	-----	-----	
ENV GENOMIC AC034203	(123)	-----	-----	
ENV GENOMIC AC018809	(70)	-----	-----	
ENV GENOMIC HERV-KI02 AF164610	(124)	-----	-----	
ENV GENOMIC FRAG. AF260253	(1)	-----	-----	
CONSENSUS	(161)	T GACTCACAAGATGAA AAAATGGTGA TCAGAAGACAGATGAAGTTGCCATCCACCAAGAA GC GA		

[illegible]

[illegible]

ENV GENOMIC HERV-MDA
ENV GENOMIC HERV-K TAN.
ENV GENOMIC AC025420
ENV GENOMIC AP000776
ENV GENOMIC HERV-K8
ENV GENOMIC HERV-KI
ENV HERV-K AF023261
ENV GEN AL035086
ENV GENOMIC AL035587
ENV GENOMIC AC012068
ENV GENOMIC AF277315
ENV GENOMIC AF027650
ENV GENOMIC AC078899
ENV GENOMIC HERV-KII
ENV GENOMIC AC008813
ENV GENOMIC AC012309
ENV GENOMIC AL121932
ENV GENOMIC AD000090
ENV GEN AL160008
ENV GENOMIC HEU32496
ENV GENOMIC AC011467
ENV GENOMIC AF235103
ENV GENOMIC AC026786
ENV GENOMIC AC034203
ENV GENOMIC AC018809
ENV GENOMIC HERV-K102 AF164410
ENV GENOMIC FRAG. AF260253
CONSISTENT

FIGURE 6 CONTD...

[illegible]

FIGURE 6 CONTD...

ENV GENOMIC HERV MDA	(820)	961	1040
ENV GENOMIC HERV-K TAN.	(846)	GGCAGAGTGTATGATGTTACAGGAGCCCTCCATCTGGCCCATTAATCCAGCTATGACGTTGTTGAAAGTGAAGGCG	
ENV GENOMIC AC025420	(843)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	AGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AP000776	(846)	GGCAAACTCAGTGGTTCGAAGTTCACAA	AGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC HERV-K8	(291)	GGCAAACTCAGTGGTTCGAAGTTCACAA	AGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC HERV-KI	(846)	GGCAAACTCAGTGGTTCGAAGTTCACAA	AGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV HERV-K AF023261	(701)	GGCAAACTCAGTGGTTCGAAGTTCACAA	AGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GEN AL035086	(632)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	AGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AL035587	(870)	GGCAGAGTGTATGATGTTACAGGAGCCCTCCATCTGGCCCATTAATCCAGCTATGACGTTGTTGAAAGTGAAGGCG	
ENV GENOMIC AC012068	(834)	GGCAGAGTGTATGATGTTACAGGAGCCCTCCATCTGGCCCATTAATCCAGCTATGACGTTGTTGAAAGTGAAGGCG	
ENV GENOMIC AF277315	(843)	GGCAGAGTGTATGATGTTACAGGAGCCCTCCATCTGGCCCATTAATCCAGCTATGACGTTGTTGAAAGTGAAGGCG	
ENV GENOMIC AF027650	(700)	GGCAGAGTGTATGATGTTACAGGAGCCCTCCATCTGGCCCATTAATCCAGCTATGACGTTGTTGAAAGTGAAGGCG	
ENV GENOMIC AC078899	(845)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC HERV-KII	(554)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AC008813	(865)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AC012309	(845)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AL121932	(843)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AD000090	(859)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GEN AL160008	(647)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC HEU32496	(441)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AC011467	(610)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AF235103	(904)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AC026786	(780)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AC034203	(886)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC AC018809	(553)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC HERV-KI02 AF164610	(606)	GTAGAAACTCAGTGGTTCGAAGTTCACAA	TGAGTCCAGCTGTGATAGGCACTTAACGAAAGTTT
ENV GENOMIC FRAG. AF260253	(1)	GG CAAATCTA TC TGTC AG GCACAG	AGTCCAGCTGTGATAG GACTTAACAGAAAGT T
CONSENSUS	(961)		
ENV GENOMIC HERV MDA	(900)	1041	1120
ENV GENOMIC HERV-K TAN.	(914)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC025420	(911)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AP000776	(914)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC HERV-K8	(291)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC HERV-KI	(914)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV HERV-K AF023261	(701)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GEN AL035086	(950)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AL035587	(914)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC012068	(923)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AF277315	(700)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AF027650	(913)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC078899	(622)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC HERV-KII	(933)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC008813	(913)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC012309	(911)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AL121932	(927)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AD000090	(647)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GEN AL160008	(441)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC HEU32496	(676)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC011467	(984)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AF235103	(860)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC026786	(966)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC034203	(621)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC AC018809	(674)	GGCAGGTTTAA--TGAAGGTTTGAATGACCTGTCGAGGAAAGGCGTGAAGGCGAATTGATGA	
ENV GENOMIC HERV-KI02 AF164610	(1)	AGAC AA T A TA AA TTA A TC TCTA CC TGG AATGGGG GAAAA GGAAT TC C	
ENV GENOMIC FRAG. AF260253	(1041)		
CONSENSUS	(1041)		
ENV GENOMIC HERV MDA	(967)	1121	1200
ENV GENOMIC HERV-K TAN.	(984)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC025420	(981)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AP000776	(984)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC HERV-K8	(291)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC HERV-KI	(984)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV HERV-K AF023261	(701)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GEN AL035086	(770)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AL035587	(1017)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC012068	(981)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AF277315	(990)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AF027650	(700)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC078899	(993)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC HERV-KII	(692)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC008813	(1003)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC012309	(983)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AL121932	(981)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AD000090	(997)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GEN AL160008	(647)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC HEU32496	(441)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC011467	(683)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AF235103	(1051)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC026786	(927)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC034203	(1033)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC AC018809	(691)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC HERV-KI02 AF164610	(744)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
ENV GENOMIC FRAG. AF260253	(1)	TTTACGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTAAGTACAGCAATTTCCGGGTTTCACCTTTCTGTGCCA	
CONSENSUS	(1121)		

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FIGURE 6 CONTD...

	1201	1280
ENV GENOMIC HERV MDA	(967)	-----
ENV GENOMIC HERV-K TAN.	(984)	-----
ENV GENOMIC AC025420	(981)	-----
ENV GENOMIC AP000776	(984)	-----
ENV GENOMIC HERV-K8	(291)	-----
ENV GENOMIC HERV-KI	(984)	-----
ENV HERV-K AF023261	(701)	-----
ENV GEN AL035086	(770)	-----
ENV GENOMIC AL035587	(1017)	-----
ENV GENOMIC AC012068	(981)	-----
ENV GENOMIC AF277315	(990)	-----
ENV GENOMIC AF027650	(700)	-----
ENV GENOMIC AC078899	(1073)	CCACCCCGACTAACGCACATGCCCACTAGGGCGTGTCACACTCAGAAGTGTGAAACTCAACCGATCCCGCCCTACCCCG
ENV GENOMIC HERV-KII	(692)	-----
ENV GENOMIC AC008813	(1003)	-----
ENV GENOMIC AC012309	(983)	-----
ENV GENOMIC AL121932	(981)	-----
ENV GENOMIC AD000090	(997)	-----
ENV GEN AL160008	(647)	-----
ENV GENOMIC HEU32496	(441)	-----
ENV GENOMIC AC011467	(683)	-----
ENV GENOMIC AF235103	(1051)	-----
ENV GENOMIC AC026786	(927)	-----
ENV GENOMIC AC034203	(1033)	-----
ENV GENOMIC AC018809	(691)	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----
ENV GENOMIC FRAG. AF260253	(1)	-----
CONSENSUS	(1201)	-----

	1281	1360
ENV GENOMIC HERV MDA	(967)	-----
ENV GENOMIC HERV-K TAN.	(984)	-----
ENV GENOMIC AC025420	(981)	-----
ENV GENOMIC AP000776	(984)	-----
ENV GENOMIC HERV-K8	(291)	-----
ENV GENOMIC HERV-KI	(984)	-----
ENV HERV-K AF023261	(701)	-----
ENV GEN AL035086	(770)	-----
ENV GENOMIC AL035587	(1017)	-----
ENV GENOMIC AC012068	(981)	-----
ENV GENOMIC AF277315	(990)	-----
ENV GENOMIC AF027650	(700)	-----
ENV GENOMIC AC078899	(1153)	ACCACTTCCTCACCCAGCATCCATAAAGCGCGCTGCACCTTTGCGCACAGCGTGACTTCCCTGGCGGACCAGTGAACCTC
ENV GENOMIC HERV-KII	(692)	-----
ENV GENOMIC AC008813	(1003)	-----
ENV GENOMIC AC012309	(983)	-----
ENV GENOMIC AL121932	(981)	-----
ENV GENOMIC AD000090	(997)	-----
ENV GEN AL160008	(647)	-----
ENV GENOMIC HEU32496	(441)	-----
ENV GENOMIC AC011467	(683)	-----
ENV GENOMIC AF235103	(1051)	-----
ENV GENOMIC AC026786	(927)	-----
ENV GENOMIC AC034203	(1033)	-----
ENV GENOMIC AC018809	(691)	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----
ENV GENOMIC FRAG. AF260253	(1)	-----
CONSENSUS	(1281)	-----

	1361	1440
ENV GENOMIC HERV MDA	(967)	-----
ENV GENOMIC HERV-K TAN.	(984)	-----
ENV GENOMIC AC025420	(981)	-----
ENV GENOMIC AP000776	(984)	-----
ENV GENOMIC HERV-K8	(291)	-----
ENV GENOMIC HERV-KI	(984)	-----
ENV HERV-K AF023261	(701)	-----
ENV GEN AL035086	(770)	-----
ENV GENOMIC AL035587	(1017)	-----
ENV GENOMIC AC012068	(981)	-----
ENV GENOMIC AF277315	(990)	-----
ENV GENOMIC AF027650	(700)	-----
ENV GENOMIC AC078899	(1233)	ACCGGAGAGCTCAATAAAGAGATTTTGGCCCTCTTTGTCTTGCCCTCTTGCCCTTATTGATCCACGGTGCCCTTCCATTG
ENV GENOMIC HERV-KII	(692)	-----
ENV GENOMIC AC008813	(1003)	-----
ENV GENOMIC AC012309	(983)	-----
ENV GENOMIC AL121932	(981)	-----
ENV GENOMIC AD000090	(997)	-----
ENV GEN AL160008	(647)	-----
ENV GENOMIC HEU32496	(441)	-----
ENV GENOMIC AC011467	(683)	-----
ENV GENOMIC AF235103	(1051)	-----
ENV GENOMIC AC026786	(927)	-----
ENV GENOMIC AC034203	(1033)	-----
ENV GENOMIC AC018809	(691)	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----
ENV GENOMIC FRAG. AF260253	(1)	-----
CONSENSUS	(1361)	-----

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FIGURE 6 CONTD...

ENV GENOMIC HERV-MDA (1190) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC HERV-K TAN. (1209) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC025420 (1206) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AP000776 (1209) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC HERV-K8 (291) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC HERV-KI (1209) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV HERV-K AF023261 (701) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GEN AL035086 (995) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AL035587 (1242) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC012068 (1202) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AF277315 (1215) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AF027650 (700) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC078899 (1549) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC HERV-KII (913) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC008813 (1228) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC012309 (1208) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AL121932 (1207) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AD000090 (1220) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GEN AL160008 (647) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC HEU32496 (441) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC011467 (883) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AF235103 (1276) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC026786 (1152) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC034203 (1258) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC AC018809 (916) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC HERV-KI02 AF164610 (969) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 ENV GENOMIC FRAG. AF260253 (1) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT
 CONSENSUS (1681) CCAGTCTCCGACACATATA ACCCTGTGAAAATGTGAGATTGCTTACTTGCATTGATTCGAACCTTTTAATTGGCAGCACCGT

1761 1840
 ENV GENOMIC HERV-MDA (1268) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC HERV-K TAN. (1287) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC025420 (1284) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AP000776 (1287) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC HERV-K8 (291) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC HERV-KI (1287) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV HERV-K AF023261 (701) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GEN AL035086 (1073) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AL035587 (1320) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC012068 (1280) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AF277315 (1293) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AF027650 (700) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC078899 (1627) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC HERV-KII (991) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC008813 (1238) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC012309 (1288) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AL121932 (1285) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AD000090 (1298) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GEN AL160008 (647) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC HEU32496 (441) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC011467 (961) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AF235103 (1354) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC026786 (1230) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC034203 (1336) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC AC018809 (992) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC HERV-KI02 AF164610 (1047) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 ENV GENOMIC FRAG. AF260253 (1) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA
 CONSENSUS (1761) ATTCTGCTGTGAGAGCAAGAGAGGCGTGTGGATCTCTTGTGTCATGACCGACGCAATGGAGAGCTTGGTATTCAGACCA

1841 1920
 ENV GENOMIC HERV-MDA (1348) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GENOMIC HERV-K TAN. (1367) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GENOMIC AC025420 (1364) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GENOMIC AP000776 (1367) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GENOMIC HERV-K8 (291) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GENOMIC HERV-KI (1291) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV HERV-K AF023261 (701) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GEN AL035086 (1153) TATTTCGACTTAAGTATTAAAGACATTTAAATGATGACATGACCAAGATTCATTTTACTTTCATGACGACGATTCGATTCAGACCA
 ENV GENOMIC AL035587 (1399) TATTTCGACTTAAGT

1921 2000

2081 2160

ENV GENOMIC HERV MDA (1586) AGACAAACTGTCATTGGATGGAGAG - GCTCATGAGCTTGATATTTTTCAGTTACAGTGGAGCAAGATACG

ENV GENOMIC HERV-K TAN. (1605) AGACAAACTGTCATTGGATGGAGAG CAGATCATGAGCAAGATACGTTCCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AC025420 (1602) AGACAAACTGTCATTGGATGGAGAG CAGGCTCATGAGCTTACAGATACGTTCCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AP000776 (1605) AGACAAACTGTCATTGGATGGAGAG CAGATCATGAGCTTACAGATACGTTCCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC HERV-K8 (291)

ENV GENOMIC HERV-KI (1605) AGACAAACTGTCATTGGATGGAGAG CAGATCATGAGCTTACAGATACGTTCCAGTTACAGTGGAGTACGATACGTT

ENV HERV-K AF023261 (701)

ENV GEN AL035086 (1392) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AL035587 (1633) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AC012068 (1598) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AF277315 (1611) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AF027650 (700)

ENV GENOMIC AC078899 (1864) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC HERV-KII (1309) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AC008813 (1238)

ENV GENOMIC AC012309 (1606) AGG- - - - -CTCATGAGCTTGAGATAGGCTCATGAGCTTACAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AL121932 (1538)

ENV GENOMIC AD000090 (1616) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GEN AL160008 (647)

ENV GENOMIC HEU32496 (441)

ENV GENOMIC AC011467 (1279) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AF235103 (1672) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AC026786 (1548) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AC034203 (1403)

ENV GENOMIC AC018809 (1309) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC AF164610 (1365) AGACAAACTGTCATTGGATGGAGAGTAGGCTGAGTGGAGCTTGGAGATCATTTTCAGTTACAGTGGAGTACGATACGTT

ENV GENOMIC FRAG. AF260253 (1)

CONSENSUS (2081) AGACAAACTGTCATTGGATGGAGAG AG CTCATGAGCTT GAA ATC TTT CAGTTACA TGTGACTGGAATACGTT

FIGURE 6 CONTD...

[illegible]

FIGURE 6 *CONTD...*

[illegible]

FIGURE 6 CONTD...

2641 2707

ENV GENOMIC HERV MDA (2136) TGATCTCTACTAA-----

ENV GENOMIC HERV-K TAN. (2146) TTTTATCTACTAA-----

ENV GENOMIC AC025420 (2143) TTTTATCTACTAA-----

ENV GENOMIC AP000776 (2146) TTTTATCTACTAA-----

ENV GENOMIC HERV-K8 (291) -----

ENV GENOMIC HERV-KI (2141) TTTTATCTACTAA-----

ENV HERV-K AF023261 (701) -----

ENV GEN AL035086 (1931) TGATCTCTACTAA-----

ENV GENOMIC AL035587 (2146) -----

ENV GENOMIC AC012068 (2138) TAAAAAGAGCTGTACTTTGAACAATT-----

ENV GENOMIC AF277315 (2152) TAACTCTTA-----

ENV GENOMIC AF027650 (700) -----

ENV GENOMIC AC078899 (2405) TCTCTCTACTTAAGAGAAATTCCTTCGCTTGAGATGCTGTAA-----

ENV GENOMIC HERV-KII (1850) TTTTCTCTACTAA-----

ENV GENOMIC AC008813 (1238) -----

ENV GENOMIC AC012309 (2133) TTTTCTCTACTCAAG-----

ENV GENOMIC AL121932 (1538) -----

ENV GENOMIC AD000090 (2157) TTTTCTCTACTAA-----

ENV GEN AL160008 (647) -----

ENV GENOMIC HEU32496 (441) -----

ENV GENOMIC AC011467 (1699) -----

ENV GENOMIC AF235103 (2212) TAAAAAGAGCTGTACTTTGAACAATTGCTTTGCTCAGATGTTGTTAATTGTAGTTTT-----

ENV GENOMIC AC026786 (2086) TAAAAAGAGCTGTACTTTAAACAATTGCTTTGCTGAGATGTTGTTAATTGTAGCTTCCCCAGCC-----

ENV GENOMIC AC034203 (1403) -----

ENV GENOMIC AC018809 (1846) TCTCTCTACTAAG-----

ENV GENOMIC HERV-KI02 AF164610 (1906) TTTTATCTCTTAAGAAAAATTCCT-----

ENV GENOMIC FRAG. AF260253 (385) TTTTCTCTACTAA-----

CONSENSUS (2641) TG TGTAC

FIGURE 7

1 60

GI_4185938_EMB_CAA76878.1 (1) ----MGQTKSKIISKYASYLSFIKILLKRGVVKVSTKNLIKLFQIIEQFCPWFPBQGT

GI_4185942_EMB_CAA76881.1 (1) ----MGQTKSKIISKYASYLSFIKILLKRGVVKVSTKNLIKLFQIIEQFCPWFPBQGT

GI_4185946_EMB_CAA76884.1 (1) ----MGQTKSKIISKYASYLSFIKILLKRGVVKVSTKNLIKLFQIIEQFCPWFPBQGT

GI_5931704_EMB_CAB56602.1 (1) ----MGQTKTKSKYASYLSFIKILLKRGVVRVSTKNLIKLFQIIEQFCPWFPBQGNL

GAG OF AB047240 (1) ----MGQTKSKTKSKYASYLSFIKILLKRGVVRVSTKNLIKLFQIIEQFCPWFPBQGT

TRANSLATION OF ORF99 (1) YKAGLQQTSKTKSKYASYLSFIKILLKRGVVRVSTKNLIKLFQIIEQFCPWFPBQGT

TRANSLATION OF G226TOP-LINK (1) ----

TRANSLATION OF G591TOP-LINK (1) ----

TRANSLATION OF LNCAP-GAG (1) ----MGQTKSKTKSKYASYLSFIKILLKRGVVRVSTKNLIKLFQIIEQFCPWFPBQGT

GAG106-135 (1) ----

GAG186-215 (1) ----

GAG46-75 (1) ----CPWFPEQGT

PDG-G1 (1) ----

PGD-G2 (1) ----

PGD-G3 (1) ----

CONSENSUS (1) CPWFPEQG L

61 120

GI_4185938_EMB_CAA76878.1 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GI_4185942_EMB_CAA76881.1 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GI_4185946_EMB_CAA76884.1 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GI_5931704_EMB_CAB56602.1 (54) DLEDWKRIKELKQAGRKGNIPLTVWNDWPIKAALEPPQTEDSVSVSDAPGSCI IDC

GAG OF AB047240 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

TRANSLATION OF ORF99 (61) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

TRANSLATION OF G226TOP-LINK (1) ----

TRANSLATION OF G591TOP-LINK (1) ----

TRANSLATION OF LNCAP-GAG (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GAG106-135 (1) ----DAPGSCI IDC

GAG186-215 (1) ----

GAG46-75 (11) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

PDG-G1 (1) ---DWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

PGD-G2 (1) ----

PGD-G3 (1) ----

CONSENSUS (61) DL DWKRIG ELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

FIGURE 7 CONTD...

GI_4185938_EMB_CAA76881.1	(116)	NENTRKKKSQKETEGHLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE	121	180
GI_4185942_EMB_CAA76881.1	(116)	NENTRKKKSQKETESLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE		
GI_4185946_EMB_CAA76884.1	(116)	NENTRKKKSQKETEGHLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE		
GI_5931704_EMB_CAB56602.1	(113)	NEKTRKKKSQKETETLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE		
GAG OF AB047240	(116)	NEKTGRKKKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIIYPETLKLEGKGPPELVGPSE		
TRANSLATION OF ORF99	(121)	NEKTGRKKKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIIYPETLKLEGKGPPELVGPSE		
TRANSLATION OF G226TOP-LINK	(1)	-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(116)	NEKTGRKKKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIIYPETLKLEGKGPPELVGPSE		
GAG106-135	(11)	NENTRKKKSQKETEGHLHCEYV-----		
GAG186-215	(1)	-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(1)	-----		
PGD-G3	(1)	-----		
CONSENSUS	(121)	NE T KKSQKETE LHCEYV		
GI_4185938_EMB_CAA76881.1	(176)	SKPRGTSPLPAGQVPVTLQPQKQV-----	181	240
GI_4185942_EMB_CAA76881.1	(176)	SKPRGTSRLPAGQVPVTLQPQKQV-----		
GI_4185946_EMB_CAA76884.1	(176)	SKPRGTSPLPAGQVPVTLQPQKQV-----		
GI_5931704_EMB_CAB56602.1	(173)	SKPRGSPSLSAGQVTVTLQPQAQV-----		
GAG OF AB047240	(176)	SKPRGSPSLPAGQVPVTLQPQKQV-----		
TRANSLATION OF ORF99	(181)	SKPRGSPSLPAGQVPVTLQPQKQV-----		
TRANSLATION OF G226TOP-LINK	(1)	-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(176)	SKPRGSPSLPAGQVPVTLQPQKQV-----		
GAG106-135	(31)	-----		
GAG186-215	(1)	-----AGQVPVTLQPQKQV-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(1)	-----		
PGD-G3	(1)	-----		
CONSENSUS	(181)	AGQV VTLQPQ QVKENKTQ PVAYQYWPP SQYGY GMPP		
GI_4185938_EMB_CAA76881.1	(236)	APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTAWQFPVTLPEMPMPGEA	241	300
GI_4185942_EMB_CAA76881.1	(236)	APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTAWQFPVTLPEMPMPGEA		
GI_4185946_EMB_CAA76884.1	(236)	APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTAWQFPVTLPEMPMPGEA		
GI_5931704_EMB_CAB56602.1	(233)	APQDREYPYPQPPTTRQCYGTT-----		
GAG OF AB047240	(236)	ALQGRAPYPQPPTVRLNPTASRSQGGLTHAVIDEARKQGDLEAWRFLVILQLVQAGEET		
TRANSLATION OF ORF99	(241)	ALQGRAPYPQPPTVRLNPTASRSQGGLTHAVIDEARKQGDLEAWRFLVILQLVQAGEET		
TRANSLATION OF G226TOP-LINK	(11)	APQGRAPYPQPPTTRLNPTA-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(236)	ALQGRAPYPQPPTVRLNPTASRSQGGLTHAVIDEARKQGDLEAWRFLVILQLVQAGEET		
GAG106-135	(31)	-----		
GAG186-215	(31)	-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(1)	-----SKLHEIIDKSRKEGDT-----		
PGD-G3	(1)	-----		
CONSENSUS	(241)	A Q R PYPQPPT R		
GI_4185938_EMB_CAA76881.1	(296)	QEGEPPTVEARYKSFISIKLKDMDKEGVKQYGNPSYMRLLDSIAHGHRILIPYDWESLAK	301	360
GI_4185942_EMB_CAA76881.1	(296)	QEGEPPTVEARYKSFISIKLKDMDKEGVKQYGNPSYMRLLDSIAHGHRILIPYDWESLAK		
GI_4185946_EMB_CAA76884.1	(296)	QEGEPPTVEARYKSFISIKLKDMDKEGVKQYGNPSYMRLLDSIAHGHRILIPYDWESLAK		
GI_5931704_EMB_CAB56602.1	(254)	-----		
GAG OF AB047240	(296)	QVGAPARAETRCPEFTMKMLKDIKEGVKQYGSNSPYIRLLDSIAHGHRILTPYDWESLAK		
TRANSLATION OF ORF99	(301)	QVGAPARAETRCPEFTMKMLKDIKEGVKQYGSNSPYIRLLDSIAHGHRILTPYDWESLAK		
TRANSLATION OF G226TOP-LINK	(31)	-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(296)	QVGAPARAETRCPEFTMKMLKDIKEGVKQYGSNSPYIRLLDSIAHGHRILTPYDWESLAK		
GAG106-135	(31)	-----		
GAG186-215	(31)	-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(17)	-----		
PGD-G3	(1)	-----		
CONSENSUS	(301)			

FIGURE 7 CONTD...

		361	420
GI_4185938_EMB_CAA76878.1_	(356)	SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA	
GI_4185942_EMB_CAA76881.1_	(356)	SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA	
GI_4185946_EMB_CAA76884.1_	(356)	SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(356)	SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA	
TRANSLATION OF ORF99	(361)	SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(356)	SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(361)	-----	
		421	480
GI_4185938_EMB_CAA76878.1_	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI	
GI_4185942_EMB_CAA76881.1_	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI	
GI_4185946_EMB_CAA76884.1_	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(416)	IEQVRAICLRAWGKIQDPGTAPP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI	
TRANSLATION OF ORF99	(421)	IEQVRAICLRAWGKIQDPGTAPP-PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(416)	IEQVRAICLRAWGKIQDPGTAPP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(421)	-----	
		481	540
GI_4185938_EMB_CAA76878.1_	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIIGGAMYKAMLMAQAITGVVL	
GI_4185942_EMB_CAA76881.1_	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGMGGAMHKAMLMAQAITGVVL	
GI_4185946_EMB_CAA76884.1_	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIIGGAMHKAMLMAQAITGVVL	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(475)	VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIIGGAMHKAMLMAQAMRGLTL	
TRANSLATION OF ORF99	(480)	VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIIGGAMHKAMLMAQAMRGLTL	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(475)	VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIIGGAMHKAMLMAQAMRGLTL	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(481)	-----	
		541	600
GI_4185938_EMB_CAA76878.1_	(536)	GGQVRTFGRKCYNCQGIGHLKKNCPLNKNQITIQATTG-REPPDLCPRCCKGKHWSAQ	
GI_4185942_EMB_CAA76881.1_	(536)	GGQVRTFGRKCYNCQGIGHLKKNCPLNKNQITIQATTG-REPPDLCPRCCKGKHWSAQ	
GI_4185946_EMB_CAA76884.1_	(536)	GGQVRTFGRKCYNCQGIGHLKKNCPLNKNQITIQATTG-REPPDLCPRCCKGKHWSAQ	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(535)	GGQVRTFGRKCYNCQGIGHLKRSCPLNKNQIINQAITAKNKKPSGLCPKCGKGKHWSAQ	
TRANSLATION OF ORF99	(540)	GGQVRTFGRKCYNCQGIGHLKRSCPLNKNQIINQAITAKNKKPSGLCPKCGKGKHWSAQ	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(535)	GGQVRTFGRKCYNCQGIGHLKRSCPLNKNQIINQAITAKNKKPSGLCPKCGKGKHWSAQ	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(541)	-----	

FIGURE 7 CONTD...

		601	660
GI_4185938_EMB_CAA76878.1_	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFIQPFVPGFGGQQP-PLSQVFQGISQLPQ	
GI_4185942_EMB_CAA76881.1_	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFIQPFVPHGFGGQQP-PLSQVFQGISQLPQ	
GI_4185946_EMB_CAA76884.1_	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFIQPFVPGFGGQQP-PLSQVFQGISQLPQ	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(595)	CHSKFDKDGQPLSGNRKRGPQAPQQTGAFFVQLFVPGFGGQQPLQKIPPLQGVSQLQQ	
TRANSLATION OF ORF99	(600)	CHSKFDKDGQPLSGNRKRGPQAPQQTGAFFVQLFVPGFGGQQPLQKIPPLQGVSQLQQ	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(5)	CRSKFDKNGQPLSGNEQRGQPQAPQ-----	
TRANSLATION OF LNCAP-GAG	(595)	CHSKFDKDGQPLSGNRKRGPQAPQQTGAFFVQLFVPGFGGQQPLQKIPPLQGVSQLQQ	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PGD-G2	(17)	-----	
PGD-G3	(1)	CRSKFDKNGQPLSGNE-----	
CONSENSUS	(601)	C SKFDK GQPLSGN	

		661	673
GI_4185938_EMB_CAA76878.1_	(654)	YNNCPPPQAAVQQ	
GI_4185942_EMB_CAA76881.1_	(654)	YNNCPPPQAAVQQ	
GI_4185946_EMB_CAA76884.1_	(654)	YNNCPPPQAAVQQ	
GI_5931704_EMB_CAB56602.1_	(254)	-----	
GAG OF AB047240	(655)	SNSCPAPQQAAPQ	
TRANSLATION OF ORF99	(660)	SNSCPAPQQAAPQ	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(31)	-----	
TRANSLATION OF LNCAP-GAG	(655)	SNSCPAPQQAAPQ	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PGD-G2	(17)	-----	
PGD-G3	(17)	-----	
CONSENSUS	(661)		

FIGURE 8

		1	60
GI_4185939_EMB_CAA76879.1_	(1)	MLTDLRAVN---AVIQPMGFLQPLGSPAMIPKDWELI IIDLKDCFFTIPLAEQDCEKFA	
GI_4185943_EMB_CAA76882.1_	(1)	MLTDLRAVNNAVNAVQPMGFLQPLGSLAMI PKDWELI IIDLKDCFFTIPLAEQDCEKFA	
GI_4185947_EMB_CAA76885.1_	(1)	MLTDLRAVN---AVIQPMGFLQPLGSPAMIPKDWELI IIDLKDCFFTIPLAEQDCEKFA	
GI_5931705_EMB_CAB56603.1_	(1)	-----MIPKDWELI IIDLKDCFFTIPLAEQDCEKFA	
ENV OF AB047240	(1)	-----	
TRANSLATION OF P386TOP-LINK	(1)	-----	
TRANSLATION OF POL349-LINK	(1)	-----	
LNCAP-GENOMEA-POLORF	(1)	-----	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	
TRANSLATION OF ORF111-10	(1)	-----	
PGD-P1	(1)	-----	
PGD-P2	(1)	-----	
PGDP3	(1)	-----	
CONSENSUS	(1)		
		61	120
GI_4185939_EMB_CAA76879.1_	(58)	FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC	
GI_4185943_EMB_CAA76882.1_	(61)	FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHYIDDILC	
GI_4185947_EMB_CAA76885.1_	(58)	FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC	
GI_5931705_EMB_CAB56603.1_	(32)	FTIPAINNKEPATRFQWKVLPQGMLNSPTLCQTFVGRALQPVREKFSDCYIIHYFDDILC	
ENV OF AB047240	(1)	-----	
TRANSLATION OF P386TOP-LINK	(1)	-----	
TRANSLATION OF POL349-LINK	(1)	-----	
LNCAP-GENOMEA-POLORF	(1)	-----	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	
TRANSLATION OF ORF111-10	(1)	-----	
PGD-P1	(1)	-----	
PGD-P2	(1)	-----	
PGDP3	(1)	-----	
CONSENSUS	(61)		

FIGURE 8 CONTD...

GI_4185939_EMB_CAA76879.1	(118)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQSTSTPPHYLGMQIENRKIKPKQKIEIRKDT	121		180
GI_4185943_EMB_CAA76882.1	(121)	AAEMKDKLIDCYTFLQAEVANAGLAIASDKIQSTSTPPHYLEMQIENRKIKPKKIEIRKDT	(121)		
GI_4185947_EMB_CAA76885.1	(118)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQSTSTPPHYLGMQIENRKIKPKQKIEIRKDT	(118)		
GI_5931705_EMB_CAB56603.1	(92)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQSTSTPPHYLGMQIENRKIKPKQKIEIRKDT	(92)		
ENV OF AB047240	(1)	-----	(1)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(1)	-----	(1)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	(1)		
TRANSLATION OF ORF111-10	(1)	-----	(1)		
PGD-P1	(1)	-----	(1)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(121)	-----	(121)		
GI_4185939_EMB_CAA76879.1	(178)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	181		240
GI_4185943_EMB_CAA76882.1	(181)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	(181)		
GI_4185947_EMB_CAA76885.1	(178)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	(178)		
GI_5931705_EMB_CAB56603.1	(152)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	(152)		
ENV OF AB047240	(1)	-----	(1)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(1)	-----	(1)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	(1)		
TRANSLATION OF ORF111-10	(1)	-----	(1)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(181)	-----	(181)		
GI_4185939_EMB_CAA76879.1	(238)	KIQSAQINRIDPLAPLOLIFTAHSPTIIQNTDLVWSFLPHSTTKTFTLYLQDMAT	241		300
GI_4185943_EMB_CAA76882.1	(241)	KIQSAQINRIDPLAPLOLIFTAHSPTIIQNTDLVWSFLPHSTTKTFTLYLQDMAT	(241)		
GI_4185947_EMB_CAA76885.1	(238)	KIQSAQINRIDPLAPLOLIFTAHSPTIIQNTDLVWSFLPHSTTKTFTLYLQDMAT	(238)		
GI_5931705_EMB_CAB56603.1	(212)	KIQSAQINRIDPLAPLOLIFTAHSPTIIQNTDLVWSFLPHSTTKTFTLYLQDMAT	(212)		
ENV OF AB047240	(1)	-----	(1)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(1)	-----	(1)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	(1)		
TRANSLATION OF ORF111-10	(1)	-----	(1)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(241)	D LAPLQLLIFATAHS TGIIIQNTDLVWSFLPHSTTKTFTLYLQDMAT	(241)		
GI_4185939_EMB_CAA76879.1	(298)	LIGQTRLRIIILCGNDPDKIVVPLTKQVROAFINSQAWKIGLANFGIIDNHYPKTKIF	301		360
GI_4185943_EMB_CAA76882.1	(301)	LIGQTRLRIIILCGNDPDKIVVPLTKQVROAFINSQAWKIGLANFGIIDNHYPKTKIF	(301)		
GI_4185947_EMB_CAA76885.1	(298)	LIGQTRLRIIILCGNDPDKIVVPLTKQVROAFINSQAWKIGLANFGIIDNHYPKTKIF	(298)		
GI_5931705_EMB_CAB56603.1	(272)	LIGQTRLRIIILCGNDPDKIVVPLTKQVROAFINSQAWKIGLANFGIIDNHYPKTKIF	(272)		
ENV OF AB047240	(4)	LIGQGRRLRIITLCGNDPDKITVPFNKQVROAFISSQAWKIGLANFGIIDNHYPKTKIF	(4)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(51)	LIGQGRRLRIITLCGNDPDKITVPFNKQVROAFISSQAWKIGLANFGIIDNHYPKTKIF	(51)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(51)	LIGQGRRLRIITLCGNDPDKITVPFNKQVROAFISSQAWKIGLANFGIIDNHYPKTKIF	(51)		
TRANSLATION OF ORF111-10	(57)	LIGQGRRLRIITLCGNDPDKITVPFNKQVROAFISSQAWKIGLANFGIIDNHYPKTKIF	(57)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(301)	LIGQ RLRII LCGNDPDKI VP K QVRQAFI SGAW IGLANFLGIIDNHYPKTKIF	(301)		
GI_4185939_EMB_CAA76879.1	(358)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	361		420
GI_4185943_EMB_CAA76882.1	(361)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(361)		
GI_4185947_EMB_CAA76885.1	(358)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(358)		
GI_5931705_EMB_CAB56603.1	(332)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(332)		
ENV OF AB047240	(64)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(64)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(10)	QFLKLTWILPKITRREP-----	(10)		
LNCAP-GENOMEA-POLORF	(111)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(111)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(111)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(111)		
TRANSLATION OF ORF111-10	(117)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(117)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(361)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAAYTGPKERVIKTPYQSAQRAELVAV	(361)		

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FIGURE 8 CONTD...

GI_4185939_EMB_CAA76879.1	(418)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFFPYI	421	480
GI_4185943_EMB_CAA76882.1	(421)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFFPYI		
GI_4185947_EMB_CAA76885.1	(418)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFFPYI		
GI_5931705_EMB_CAB56603.1	(392)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFFPYI		
ENV OF AB047240	(124)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFFPYI		
TRANSLATION OF P386TOP-LINK	(31)	-----		
TRANSLATION OF POL349-LINK	(28)	-----		
LNCAP-GENOMEA-POLORF	(171)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFFPYI		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(171)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFFPYI		
TRANSLATION OF ORF111-10	(177)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFFPYI		
PGD-P1	(17)	-----		
PGD-P2	(17)	-----		
PGDP3	(1)	-----		
CONSENSUS	(421)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYS DD LNQLFNLLQQTVRKRNFFPYI		
GI_4185939_EMB_CAA76879.1			481	540
GI_4185943_EMB_CAA76882.1	(478)	THIRAHNTLPGPLTKANEQADLLVSSALIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV		
GI_4185947_EMB_CAA76885.1	(481)	THIRAHNTLPGPLTKANEQADLLVSSALIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV		
GI_5931705_EMB_CAB56603.1	(478)	THIRAHNTLPGPLTKANEQADLLVSSALIKAEQLHALAHVNAAGLKNKFDVTWKQAKDIV		
ENV OF AB047240	(452)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV		
TRANSLATION OF P386TOP-LINK	(184)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
TRANSLATION OF POL349-LINK	(31)	-----		
LNCAP-GENOMEA-POLORF	(28)	-----		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(231)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
TRANSLATION OF ORF111-10	(231)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
PGD-P1	(237)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
PGD-P2	(17)	-----		
PGDP3	(17)	-----		
CONSENSUS	(1)	-----		
	(481)	THIRAHNTLPGPLTKANEQADLLVSSA IKAQL ALTHVNAAGLKNKFDVTWKQAKDIV		
GI_4185939_EMB_CAA76879.1			541	600
GI_4185943_EMB_CAA76882.1	(538)	QHCTCQCVLHLPTQEBAGVNPRLGCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC		
GI_4185947_EMB_CAA76885.1	(541)	QHCTCQCVLHLPTQEBAGVNPRLGCPNALWQMDVTHVSSFGRLSYVHVTVDTYSHFIWATC		
GI_5931705_EMB_CAB56603.1	(538)	QHCTCQCVLHLPTQEBAGVNPRLGCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC		
ENV OF AB047240	(512)	QHCTCQCVLDLPTQEBAGVNPRLGCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC		
TRANSLATION OF P386TOP-LINK	(244)	QHCTCQCVLHLSTQEBAGVNPRLGCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC		
TRANSLATION OF POL349-LINK	(31)	-----		
LNCAP-GENOMEA-POLORF	(28)	-----		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(291)	QHCTCQCVLHLSTQEBAGVNPRLGCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC		
TRANSLATION OF ORF111-10	(291)	QHCTCQCVLHLSTQEBAGVNPRLGCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC		
PGD-P1	(297)	QHCTCQCVLHLSTQEBAGVNPRLGCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC		
PGD-P2	(17)	-----		
PGDP3	(17)	-----		
CONSENSUS	(1)	-----		
	(541)	QHCTCQCVLHL TQEBAGVNPRLGCPNALWQMD THV SFGRLSYVHVTVDTYSHFIWATC		
GI_4185939_EMB_CAA76879.1			601	660
GI_4185943_EMB_CAA76882.1	(598)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
GI_4185947_EMB_CAA76885.1	(601)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
GI_5931705_EMB_CAB56603.1	(598)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
ENV OF AB047240	(572)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
TRANSLATION OF P386TOP-LINK	(304)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
TRANSLATION OF POL349-LINK	(31)	-----		
LNCAP-GENOMEA-POLORF	(28)	-----		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(351)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
TRANSLATION OF ORF111-10	(351)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
PGD-P1	(357)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
PGD-P2	(17)	-----		
PGDP3	(17)	-----		
CONSENSUS	(1)	-----		
	(601)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
GI_4185939_EMB_CAA76879.1			661	720
GI_4185943_EMB_CAA76882.1	(658)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
GI_4185947_EMB_CAA76885.1	(661)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
GI_5931705_EMB_CAB56603.1	(658)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
ENV OF AB047240	(632)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAE-HLT		
TRANSLATION OF P386TOP-LINK	(364)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
TRANSLATION OF POL349-LINK	(31)	-----		
LNCAP-GENOMEA-POLORF	(28)	-----		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(411)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
TRANSLATION OF ORF111-10	(411)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
PGD-P1	(417)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
PGD-P2	(17)	-----		
PGDP3	(17)	-----		
CONSENSUS	(1)	-----		
	(661)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSA QHLT		

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FIGURE 8 CONTD...

GI_4185939_EMB_CAA76879.1	(718)	GKKNSPHEGKLIWWKDSKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	721		780
GI_4185943_EMB_CAA76882.1	(721)	GKKNSPHEGKLIWWKDNKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(721)		
GI_4185947_EMB_CAA76885.1	(718)	GKKNSPHEGKLIWWKDNKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(718)		
GI_5931705_EMB_CAB56603.1	(691)	GKKNSPHEGKLI-----	(691)		
ENV OF AB047240	(424)	GKKHSPHEGKLIWWKDNKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(424)		
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)		
TRANSLATION OF POL349-LINK	(28)	-----	(28)		
LNCAP-GENOMEA-POLORF	(471)	GKKHSPHEGKLIWWKDNKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(471)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(471)	GKKHSPHEGKLIWWKDNKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(471)		
TRANSLATION OF ORF111-10	(477)	GKKHSPHEGKLIWWKDNKNKTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(477)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(17)	-----	(17)		
PGDP3	(4)	GKKNSPHEGKLI-----	(4)		
CONSENSUS	(721)	GKK SPHEGKLIWWKD KNTWEIGKVIITWGRGFACVSPGENQLPVWIPTRHLKIFYNEPI	(721)		
GI_4185939_EMB_CAA76879.1	(778)	RDAAKSTSAETETS-----	781		840
GI_4185943_EMB_CAA76882.1	(781)	GDAKKSTSAETETP-----	(781)		
GI_4185947_EMB_CAA76885.1	(778)	RDAAKSTSAETETS-----	(778)		
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)		
ENV OF AB047240	(484)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVVPGPTDDRCAPKPEEEGMMINISIVYRYP	(484)		
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)		
TRANSLATION OF POL349-LINK	(28)	-----	(28)		
LNCAP-GENOMEA-POLORF	(531)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVVPGPTDDRCAPKPEEEGMMINISIVYRYP	(531)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(531)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVVPGPTDDRCAPKPEEEGMMINISIVYRYP	(531)		
TRANSLATION OF ORF111-10	(537)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVVPGPTDDRCAPKPEEEGMMINISIVYRYP	(537)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(17)	-----	(17)		
PGDP3	(17)	-----	(17)		
CONSENSUS	(781)	DAAK S E T	(781)		
GI_4185939_EMB_CAA76879.1	(792)	-----	841		900
GI_4185943_EMB_CAA76882.1	(795)	-----	(795)		
GI_4185947_EMB_CAA76885.1	(792)	-----	(792)		
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)		
ENV OF AB047240	(544)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(544)		
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)		
TRANSLATION OF POL349-LINK	(28)	-----	(28)		
LNCAP-GENOMEA-POLORF	(591)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(591)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(591)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(591)		
TRANSLATION OF ORF111-10	(597)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(597)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(17)	-----	(17)		
PGDP3	(17)	-----	(17)		
CONSENSUS	(841)	-----	(841)		
GI_4185939_EMB_CAA76879.1	(792)	-----	901		960
GI_4185943_EMB_CAA76882.1	(795)	-----	(795)		
GI_4185947_EMB_CAA76885.1	(792)	-----	(792)		
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)		
ENV OF AB047240	(604)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(604)		
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)		
TRANSLATION OF POL349-LINK	(28)	-----	(28)		
LNCAP-GENOMEA-POLORF	(651)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(651)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(651)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(651)		
TRANSLATION OF ORF111-10	(657)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(657)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(17)	-----	(17)		
PGDP3	(17)	-----	(17)		
CONSENSUS	(901)	-----	(901)		
GI_4185939_EMB_CAA76879.1	(816)	QEGRAANLCTTKKADAVSYKISREHKGDTNPREACSDDCINGGKSPYCRSSCS---	961		1020
GI_4185943_EMB_CAA76882.1	(819)	QESRAADLCTTKKADAVSYKISREHKGDTNPREACSDDCINGGKSPYCRSSCS---	(819)		
GI_4185947_EMB_CAA76885.1	(816)	QEGRAANLCTTKKADAVSYKISREHKGDTNPREACSDDCINGGKSPYCRSSCS---	(816)		
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)		
ENV OF AB047240	(664)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGKGSTPRPEIISPVGPEHPFELWR	(664)		
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)		
TRANSLATION OF POL349-LINK	(28)	-----	(28)		
LNCAP-GENOMEA-POLORF	(711)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGKGSTPRPEIISPVGPEHPFELWR	(711)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(711)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGKGSTPRPEIISPVGPEHPFELWR	(711)		
TRANSLATION OF ORF111-10	(717)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGKGSTPRPEIISPVGPEHPFELWR	(717)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(17)	-----	(17)		
PGDP3	(17)	-----	(17)		
CONSENSUS	(961)	A D K P EWG I SP S	(961)		

FIGURE 8 CONTD...

	1021	1035
GI_4185939_EMB_CAA76879.1	(873)	-----
GI_4185943_EMB_CAA76882.1	(876)	-----
GI_4185947_EMB_CAA76885.1	(873)	-----
GI_5931705_EMB_CAB56603.1	(703)	-----
ENV OF AB047240	(724)	LWPDTTLEFGLEIKL
TRANSLATION OF P386TOP-LINK	(31)	-----
TRANSLATION OF POL349-LINK	(28)	-----
LNCAp-GENOMEA-POLORF	(764)	-----
TRANSLATION OF LNCAp-POL-GENA-GOODA	(771)	LWPDTTLEFGLEIKL
TRANSLATION OF ORF111-10	(777)	LWPDTTLEFGLEIKL
PGD-P1	(17)	-----
PGD-P2	(17)	-----
FGDP3	(17)	-----
CONSENSUS	(1021)	-----

FIGURE 9

	1	60
GI_4185940_EMB_CAA76880.1	(1)	-----
GI_4185944_EMB_CAA76883.1	(1)	-----
GI_4185948_EMB_CAA76886.1	(1)	-----
GI_5931706_EMB_CAB56604.1	(1)	-----
ENV OF AB047240	(1)	MATLIQGRLRIITLCGNDPDKITVPFNKQQRQAFISSGAWQIGLANFLGIIDNHYPKT
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(1)	-----

	61	120
GI_4185940_EMB_CAA76880.1	(1)	-----
GI_4185944_EMB_CAA76883.1	(1)	-----
GI_4185948_EMB_CAA76886.1	(1)	-----
GI_5931706_EMB_CAB56604.1	(1)	-----
ENV OF AB047240	(61)	KIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAEL
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(61)	-----

		121	180
GI_4185940_EMB_CAA76880.1	(1)	-----	-----
GI_4185944_EMB_CAA76883.1	(1)	-----	-----
GI_4185948_EMB_CAA76886.1	(1)	-----	-----
GI_5931706_EMB_CAB56604.1	(1)	-----	-----
ENV OF AB047240	(121)	VAVITVLQDFDQPINIISDSAYVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNF	
TRANSLATION OF E207TOP-LINK	(1)	-----	-----
TRANSLATION OF ENV287-LINK	(1)	-----	-----
TRANSLATION OF T20.22A-23	(1)	-----	-----
PGD-E1	(1)	-----	-----
PGD-E2	(1)	-----	-----
PGD-E3	(1)	-----	-----
CONSENSUS	(121)	-----	-----

81 240

		421		480
GI_4185940_EMB_CAA76880.1	(35)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQT	PESMLLAALMIVSMVVSLPMPAGAAAA	
GI_4185944_EMB_CAA76883.1	(35)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQT	PESMLLAALMIVSMVVSLPMPAGAAAA	
GI_4185948_EMB_CAA76886.1	(35)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQT	PESMLLAALMIVSMVVSLPMPAGAAAA	
GI_5931706_EMB_CAB56604.1	(1)	-----		
ENV OF AB047240	(421)	HLTGKKHSPHBGKLIWWKDNKNKTWEIGKVI	TWGRGFACVSPGENQLPVVWIPTRHLKFYN	
TRANSLATION OF E207TOP-LINK	(1)	-----		
TRANSLATION OF ENV287-LINK	(1)	-----		
TRANSLATION OF T20.22A-23	(40)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQT	PESMLLAALMIVSMVVSLPMPAGAAAA	
PGD-E1	(1)	-----		
PGD-E2	(1)	-----		
PGD-E3	(1)	-----		
CONSENSUS	(421)			

FIGURE 9 CONTD...

GI_4185940_EMB_CAA76880.1_ (95) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPIDDRCPAKPEEGBMMINISIGY 540
 GI_4185944_EMB_CAA76883.1_ (95) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPTDDHCPAKPEEGBMMINISIGY
 GI_4185948_EMB_CAA76886.1_ (95) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPIDDRCPAKPEEGBMMINISIGY
 GI_5931706_EMB_CAB56604.1_ (1) -----
 ENV OF AB047240 (481) EPIGDAKKRASTE~~MT~~PTVTWMDNPTEVYVNDVSVWVPGPTDDRCAPAKPEEGBMMINISIVY
 TRANSLATION OF E207TOP-LINK (1) -----
 TRANSLATION OF ENV287-LINK (1) -----
 TRANSLATION OF T20.22A-23 (100) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPIDDRCPAKPEEGBMMINISIGY
 PGD-E1 (1) -----
 PGD-E2 (1) -----
 PGD-E3 (1) -----
 CONSENSUS (481) LI VTWMDNP EVYVNDVSVWVPGP DD CPAKPEEGBMMINISI Y

GI_4185940_EMB_CAA76880.1_ (154) HYPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSPICRFTYHVMVSGMSLRPRVNYLQDFSQYRSL 541
 GI_4185944_EMB_CAA76883.1_ (154) RYPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSPISRFTYHVMVSGMSLRPRVNYLQDFSQYRSL 600
 GI_4185948_EMB_CAA76886.1_ (154) HYPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSPICRFTYHVMVSGMSLRPRVNYLQDFSQYRSL
 GI_5931706_EMB_CAB56604.1_ (48) HYPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSL
 ENV OF AB047240 (541) RYPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSL
 TRANSLATION OF E207TOP-LINK (1) -----
 TRANSLATION OF ENV287-LINK (1) -----
 TRANSLATION OF T20.22A-23 (159) HYPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSPICRFTYHVMVSGMSLRPRVNYLQDFSQYRSL
 PGD-E1 (1) -----
 PGD-E2 (1) -----
 PGD-E3 (1) -----
 CONSENSUS (541) YPPICLGRAPGCM~~PA~~PAVQNLVEVPTVSP RFTYHVMVSGMSLRPRVN LQDFSQYRSL

GI_4185940_EMB_CAA76880.1_ (214) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ 601
 GI_4185944_EMB_CAA76883.1_ (214) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ 660
 GI_4185948_EMB_CAA76886.1_ (214) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ
 GI_5931706_EMB_CAB56604.1_ (108) KFRPKGKTCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ
 ENV OF AB047240 (601) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ
 TRANSLATION OF E207TOP-LINK (8) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ
 TRANSLATION OF ENV287-LINK (1) -----
 TRANSLATION OF T20.22A-23 (219) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS~~AV~~ILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ
 PGD-E1 (1) -----
 PGD-E2 (1) -----
 PGD-E3 (1) -----
 CONSENSUS (601) KFRPKGKPCPK~~KE~~IPKESKNT~~EV~~LWEECVANS VILQNN~~EF~~GTTIDWAPRGQFYHNCSSGQ

GI_4185940_EMB_CAA76880.1_ (274) TQSCPSAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRPKI~~SP~~VSGPEHPE 661
 GI_4185944_EMB_CAA76883.1_ (274) TQSCPSAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRPKI~~SP~~VSGPEHPE 720
 GI_4185948_EMB_CAA76886.1_ (274) TQSCPSAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRPKI~~SP~~VSGPEHPE
 GI_5931706_EMB_CAB56604.1_ (168) TQSCPSAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRPKI~~SP~~VSGPEHPE
 ENV OF AB047240 (661) TQSCPSAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRPKI~~SP~~VSGPEHPE
 TRANSLATION OF E207TOP-LINK (31) -----
 TRANSLATION OF ENV287-LINK (1) -----
 TRANSLATION OF T20.22A-23 (279) TQSCPSAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRPKI~~SP~~VSGPEHPE
 PGD-E1 (17) -----
 PGD-E2 (1) -----
 PGD-E3 (1) -----
 CONSENSUS (661) TQSC SAQVSPA~~VD~~SDLTESLDKHKHKKLQSFY~~P~~WEGEKGISTPRP IISPVSGPEHPE

GI_4185940_EMB_CAA76880.1_ (334) LWRLTVASHHIR~~W~~SGNQ~~T~~LET~~R~~DRKPFY~~T~~IDLN~~SS~~ITVPLQSC~~K~~KPPYMLVVGNI~~V~~IKP 721
 GI_4185944_EMB_CAA76883.1_ (334) LWRLTVASHHIR~~W~~SGNQ~~T~~LET~~R~~DRKPFY~~T~~IDLN~~SS~~ITVPLQSC~~K~~KPPYMLVVGNI~~V~~IKP 780
 GI_4185948_EMB_CAA76886.1_ (334) LWRLTVASHHIR~~W~~SGNQ~~T~~LET~~R~~DRKPFY~~T~~IDLN~~SS~~ITVPLQSC~~K~~KPPYMLVVGNI~~V~~IKP
 GI_5931706_EMB_CAB56604.1_ (228) LWRLTVASHHIR~~W~~SGNQ~~T~~LET~~R~~DRKPFY~~T~~IDLN~~SS~~ITVPLQSC~~K~~KPPYMLVVGNI~~V~~IKP
 ENV OF AB047240 (721) LW-----
 TRANSLATION OF E207TOP-LINK (31) -----
 TRANSLATION OF ENV287-LINK (29) -----
 TRANSLATION OF T20.22A-23 (339) LWRLTVASHHIR~~W~~SGNQ~~T~~LET~~R~~DRKPFY~~T~~IDLN~~SS~~ITVPLQSC~~K~~KPPYMLVVGNI~~V~~IKP
 PGD-E1 (17) -----
 PGD-E2 (1) -----
 PGD-E3 (1) -----
 CONSENSUS (721) LW RI LNS LTVPLQSCVKP

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FIGURE 9 CONTD...

GI_4185940_EMB_CAA76880.1_	(394)	781	840
GI_4185944_EMB_CAA76883.1_	(394)	DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWEASPSVHILTEVLKG	
GI_4185948_EMB_CAA76886.1_	(394)	DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWEASPSVHILTEVLKG	
GI_5931706_EMB_CAB56604.1_	(288)	ASQTITCENCRLFTCTIDSTFNQHRILLVRAREGMWIPVSTDRPWEASPSIHLTEILKG	
ENV OF AB047240	(727)	-----DITLLEFGLLEIKL-----	
TRANSLATION OF E207TOP-LINK	(31)	-----	
TRANSLATION OF ENV287-LINK	(29)	-----	
TRANSLATION OF T20.22A-23	(399)	DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWEASPSVHILTEVLKG	
PGD-E1	(17)	-----	
PGD-E2	(17)	-----	
PGD-E3	(1)	-----	
CONSENSUS	(781)	DST W I L	
GI_4185940_EMB_CAA76880.1_	(454)	841	900
GI_4185944_EMB_CAA76883.1_	(454)	VLNRSKRFIPTLIAVINGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI	
GI_4185948_EMB_CAA76886.1_	(454)	VLNRSKRFIPTLIAVINGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI	
GI_5931706_EMB_CAB56604.1_	(348)	VLNRSKRFIPTLIAVINGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTRLWNSQSSI	
ENV OF AB047240	(739)	-----	
TRANSLATION OF E207TOP-LINK	(31)	-----	
TRANSLATION OF ENV287-LINK	(29)	-----	
TRANSLATION OF T20.22A-23	(459)	VLNRSKRFIPTLIAVINGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI	
PGD-E1	(17)	-----	
PGD-E2	(17)	-----	
PGD-E3	(1)	-----	
CONSENSUS	(841)		
GI_4185940_EMB_CAA76880.1_	(514)	901	960
GI_4185944_EMB_CAA76883.1_	(514)	DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH	
GI_4185948_EMB_CAA76886.1_	(514)	DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH	
GI_5931706_EMB_CAB56604.1_	(408)	DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH	
ENV OF AB047240	(739)	-----	
TRANSLATION OF E207TOP-LINK	(31)	-----	
TRANSLATION OF ENV287-LINK	(29)	-----	
TRANSLATION OF T20.22A-23	(519)	DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH	
PGD-E1	(17)	-----	
PGD-E2	(17)	-----	
PGD-E3	(1)	-----	
CONSENSUS	(901)		
GI_4185940_EMB_CAA76880.1_	(574)	961	1020
GI_4185944_EMB_CAA76883.1_	(574)	LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI	
GI_4185948_EMB_CAA76886.1_	(574)	LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI	
GI_5931706_EMB_CAB56604.1_	(468)	LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI	
ENV OF AB047240	(739)	-----	
TRANSLATION OF E207TOP-LINK	(31)	-----	
TRANSLATION OF ENV287-LINK	(29)	-----	
TRANSLATION OF T20.22A-23	(579)	LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI	
PGD-E1	(17)	-----	
PGD-E2	(17)	-----	
PGD-E3	(1)	-----	
CONSENSUS	(961)		
GI_4185940_EMB_CAA76880.1_	(634)	1021	1081
GI_4185944_EMB_CAA76883.1_	(634)	INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV	
GI_4185948_EMB_CAA76886.1_	(634)	INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV	
GI_5931706_EMB_CAB56604.1_	(528)	INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV	
ENV OF AB047240	(739)	-----	
TRANSLATION OF E207TOP-LINK	(31)	-----	
TRANSLATION OF ENV287-LINK	(29)	-----	
TRANSLATION OF T20.22A-23	(639)	INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV	
PGD-E1	(17)	-----	
PGD-E2	(17)	-----	
PGD-E3	(1)	-----	
CONSENSUS	(1021)	RCTQQLRRSDHRRERA- RCTQQLRRSD	